

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:22:07 ; Search time 88.16 Seconds
(without alignments)
26.590 Million cell updates/sec

Title: US-09-331-631A-37

Perfect score: 52
Sequence: 1 CXXCXXXXXXXXXXCXXC 20

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_15:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	46	4 Q16861	Q16861 homo sapien
2	52	100.0	47	5 Q9V1Y8	Q9V1Y8 drosophila
3	52	100.0	48	2 Q9RFP5	Q9RFP5 mycoplasma
4	52	100.0	48	6 P79377	P79377 sus scrofa
5	52	100.0	48	6 P79380	P79380 sus scrofa
6	52	100.0	49	5 Q23947	Q23947 drosophila
7	52	100.0	49	5 Q23948	Q23948 drosophila
8	52	100.0	54	13 Q9Y110	Q9Y110 bungarus mu
9	52	100.0	57	5 Q9N9H2	Q9N9H2 ruditapes p
10	52	100.0	59	5 P82107	P82107 hirudo medi
11	52	100.0	59	5 Q9N9H1	Q9N9H1 ruditapes d
12	52	100.0	60	13 Q92044	Q92044 cypripodon
13	52	100.0	60	13 Q73914	Q73914 notiothenia
14	52	100.0	60	13 Q93593	Q93593 chaenocepha
15	52	100.0	60	13 Q93609	Q93609 trematomus
16	52	100.0	60	13 Q13259	Q13259 chionodraco
17	52	100.0	60	13 Q13258	Q13258 chionodraco
18	52	100.0	60	13 Q91B50	Q91B50 pagrus majo
19	52	100.0	60	13 Q91910	Q91910 cyprinus ca

20	52	100.0	61	6 Q18842	Q18842 balaeana mys
21	52	100.0	61	6 P79431	P79431 sus scrofa
22	52	100.0	61	6 P79376	P79376 sus scrofa
23	52	100.0	61	6 P79378	P79378 sus scrofa
24	52	100.0	61	6 P79379	P79379 sus scrofa
25	52	100.0	61	6 P79375	P79375 sus scrofa
26	52	100.0	61	6 Q9XST5	Q9XST5 canis famill
27	52	100.0	62	6 Q9T015	Q9T015 canis famill
28	52	100.0	70	13 P82662	P82662 ophiophagus
29	52	100.0	71	5 Q76957	Q76957 lumbricus t
30	52	100.0	71	10 Q91RED	Q91RED brassica ca
31	52	100.0	71	10 Q91RED	Q91RED brassica ca
32	52	100.0	72	5 Q9V1Y9	Q9V1Y9 drosophila
33	52	100.0	72	6 Q28592	Q28592 ovis aries
34	52	100.0	73	5 Q76953	Q76953 lumbricus c
35	52	100.0	73	5 Q9U569	Q9U569 perna virid
36	52	100.0	73	5 Q9U568	Q9U568 perna virid
37	52	100.0	74	13 Q9Y113	Q9Y113 bungarus mu
38	52	100.0	74	13 Q9Y112	Q9Y112 bungarus mu
39	52	100.0	74	13 Q9Y111	Q9Y111 bungarus mu
40	52	100.0	74	13 Q9Y109	Q9Y109 bungarus mu
41	52	100.0	74	13 Q9Y108	Q9Y108 bungarus mu
42	52	100.0	74	13 Q9Y107	Q9Y107 bungarus mu
43	52	100.0	74	13 Q9Y106	Q9Y106 bungarus mu
44	52	100.0	74	13 Q9Y105	Q9Y105 bungarus mu
45	52	100.0	75	5 Q96858	Q96858 hirudo nipp

ALIGNMENTS

RESULT 1
ID Q16861 PRELIMINARY; PRT; 46 AA.
AC Q16861
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE CYSTEINE-RICH PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lemasson I., Devaux C., Mesnard J.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63332; AAB05810.1; -.
FT NON_TER
FT 1
SQ SEQUENCE 46 AA; 5061 MW; 311922FE40A4E8F CRC64;

Query Match 100.0%; Score 52; DB 4; Length 46;
Best Local Similarity 20.0%; Pred. No. 78;
Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXCXXXXXXXXXXCXXC 20
Db 11 CCCCCCCCCCCCCCCCCC 30

RESULT 2
ID Q9V1Y8 PRELIMINARY; PRT; 47 AA.
AC Q9V1Y8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CG17567 PROTEIN.
GN CG17567.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC	Ephydroidea: Drosophilidae: Drosophila.
OX	NcBI_TaxID=7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-BERKELEY;
RX	MEDLINE-20196006; PubMed-10731132;
RA	Adams M.D., Gelinkler S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA	Gutoge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA	Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer B.D.,
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
RA	Abriel J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA	Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA	Dudin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA	Foster C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glasser K.,
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeigbam C.,
RA	Jatalai M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA	Liu X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA	Merkulov G., Milhina N.V., Mobarry C., Morris J., Moshrefi A.,
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA	Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pachet J.M.,
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA	Reinhart K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA	Svirskas R., Teector C., Turner R., Venter E., Wang A.H., Wang X.,
RA	Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RL	"The genome sequence of <i>Drosophila melanogaster</i> .";
DR	Science 287:2185-2195(2000).
DR	EMB1: AE003662; AAES3773.1;-
DR	FLYBASE: FBgn0040994; CG17567.
SO	SEQUENCE 47 AA: 4909 MW: 19478884B86D52 CRC64;

Query Match	100.0%;	Score 52;	DB 5;	Length 47;
Best Local Similarity	20.0%;	Pred. No. 79;		
Matches 4;	Conservative 16;	Mismatches 0;	Indels 0;	Gaps 0

OY	1	CXXXCXXXXXXXXXXCXXXC 20
Db	2	CCGPGCGPCDDCGGCYCNC 21

RESULT	3		
Q9RFP5	PRELIMINARY:	PRT:	48 AA.
AC	Q9RFP5:		
DT	01-MAY-2000 (TREMBlrel. 13, Created)		
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)		
DE	ORE2.		
OS	Mycoplasmata fermentans.		
OC	Bacteria; Firmicutes; Bacillus/clostridium_group; Mollicutes;		
OC	Mycoplasmataceae; Mycoplasma.		
OX	NCBI_TaxID=2115;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-PG18;		

RA	Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;	100.0%;	Score 52;	DB 2;	Length 48;
RA	Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;	Best Local Similarity	20.0%;	Pred. No. 80;	
RT	"Differential posttranslational processing confers intraspecies	Matches	4;	Conservative	16;
RT	variation of a major surface lipoprotein and a macrophage-activating			Mismatches	0;
RT	lipopeptide of Mycoplasma fermentans.";			Indels	0;
RL	Infect. Immun. 67:760-771(1999).			Gaps	0;
RL	[2]				
RC	SEQUENCE FROM N.A.				
RC	STRAIN=PG18;				
RA	Calcutt M.J., Lavarier J.L., Wise K.S.;				
RT	"161630 of Mycoplasma fermentans, a novel IS30-type insertion element				
RT	that targets and duplicates inverted repeats of variable length and				
RT	sequence during insertion.";				
RL	J. Bacteriol. 181:7597-7607(1999).				
DR	EMBL, AF179376; AAF15567.1; -				
SO	SEQUENCE	48 AA;	5319 MW;	668836FA3592B2C7	CRC64;

QY	1 CXXCXXXXXXXXXXCXXC 20	100.0%;	Score 52;	DB 2;	Length 48;	
Db	18 CATKCTKDCCKNSCCSSC 37	Best Local Similarity	20.0%;	Pred. No. 80;		
	Matches	4;	Conservative	16;	Mismatches	0;
				Indels	0;	
				Gaps	0;	

RESULT	4				
P79377	PRELIMINARY;	PRT;	48 AA.		
ID	P79377				
AC	P79377;				
DT	01-MAY-1997 (TREMBLrel. 03, Created)				
DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)				
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)				
DE	METALLOTHIONEIN (MT) (FRAGMENT).				
OS	Sus scrofa (Pig).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
OX	NCBI_TaxID=9823;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=LIVER;				
RX	MEDLINE=98241500; PubMed=9573337;				
RA	Huang M.C., Pan P.K., Zeng T.-F., Chen N.C., Peng J.Y., Huang P.C.;				
RT	"Multiple isoforms of metallothionein are expressed in the porcine				
RT	liver.";				
RL	Gene 211:49-55(1998).				
CC	-I- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE				
CC	RESIDUES THAT BIND VARIOUS HEAVY METALS; THESE PROTEINS ARE				
CC	TRANSCRYPTICALLY REGULATED BY BOTH HEAVY METALS AND				
CC	GLUCOCORTICOIDS.				
CC	EMBL; AB000789; BAA19179.1; -				
DR	HSSP; P02795; IMHU.				
DR	INTERPRO; IPR0003019; -				
DR	INTERPRO; IPR0003019; -				
DR	PFAM; PF00131; metalthio, 1.				
DR	PRINTS; PR00860; MTEVERBATE.				
DR	PROSITE; PS00203; METALLOTHIONEIN_VRT. 1.				
KW	Metal-binding; Metal-thiolate cluster; Chelation; zinc.				
FT	NON_TER	48			
FT	METAL	24			
FT	METAL	24			
FT	METAL	27			
FT	METAL	17			
FT	METAL	19			
FT	METAL	22			
FT	METAL	31			
SO	SEQUENCE	48 AA;	4704 MW;	F0F5AC96BB9EBD19	CRC64;

Query Match	100.0%;	Score 52;	DB 6;	Length 48;	
Best Local Similarity	20.0%;	Pred. No. 80;			
Matches	4;	Conservative	16;	Mismatches	0;
				Indels	0;
				Gaps	0;

QY 1 CXXXCXXXXXXXXXXC 20
 Db 29 CKSCSCCPAGCAKCAQGC 48

RESULT 5
 ID P79380 PRELIMINARY; PRT; 48 AA.

AC P79380;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, last annotation update)
 DE METALLOTHIONEIN (MT) (FRAGMENT).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=98241500; PubMed=9573337;
 RA Huang M.C., Pan P.K., Zeng T.-F., Chen N.C., Peng J.Y., Huang P.C.;
 RT "Multiple isoforms of metallothionein are expressed in the porcine
 liver.";
 RL Gene 211:49-55(1998).
 CC -!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
 CC RESIDUES THAT BIND VARIOUS HEAVY METALS; THESE PROTEINS ARE
 CC TRANSCRIPTIONALLY REGULATED BY BOTH HEAVY METALS AND
 CC GLUCOCORTICOIDS.
 CC EMBL: AB000795; BAI1984.1; -;
 DR HSSP: P02795; 2MHU.
 DR INTERPRO: IPR000006; -;
 DR PFAM: PF00131; metalho; 1.
 DR PRINTS: PR00860; MVERTEBRATE.
 DR PROSITE: PS00203; METALLOTHIONEIN_VRT; 1.
 KW Metal-binding; Metal-chelate cluster; Chelation; Zinc.
 FT NON_TER 48 48
 FT METAL 24 24 CLUSTER.
 FT METAL 27 27 CLUSTER.
 FT METAL 17 17 CLUSTER.
 FT METAL 19 19 CLUSTER.
 FT METAL 22 22 CLUSTER.
 FT METAL 31 31 CLUSTER.
 SO SEQUENCE 48 AA; 4727 MW; 3BC2E2EBE0686216 CRC64;

Query Match 100.0%; Score 52; DB 6; Length 48;
 Best Local Similarity 20.0%; Pred. No. 80;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXCXXXXXXXXXXC 20
 Db 29 CKSCSCCPAGCAKCAQGC 48

RESULT 6
 ID Q23947 PRELIMINARY; PRT; 49 AA.

AC Q23947;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, last annotation update)
 DE TESTIS-SPECIFIC RNA.
 GN DHRC3.
 OS Drosophila hydei (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7224;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kuehn A., Buennemann H.;

RL Submitted (DEC-1990) to the EMBL/GenBank/DBJ databases.
 DR EMBL: X58114; CAA41117.1; -;
 DR FLYBASE: FBgn0015096; Dhyd\Mst87fa.
 DR INTERPRO: IPR001450; -;
 DR PROSITE: PS00198; 4FEAS_FERRDOXIN; UNKNOWN_1.
 SO SEQUENCE 49 AA; 4610 MW; BE158FEC51369F01 CRC64;

Query Match 100.0%; Score 52; DB 5; Length 49;
 Best Local Similarity 20.0%; Pred. No. 81;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXCXXXXXXXXXXC 20
 Db 23 CCGPCVSCGPGVSCCGGCC 42

RESULT 7
 ID Q23948 PRELIMINARY; PRT; 49 AA.

AC Q23948;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, last annotation update)
 DE TESTIS-SPECIFIC RNA.
 GN DHRC2.
 OS Drosophila hydei (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7224;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kuehn A., Buennemann H.;
 RL Submitted (DEC-1990) to the EMBL/GenBank/DBJ databases.
 DR EMBL: X58114; CAA41118.1; -;
 DR FLYBASE: FBgn0015097; Dhyd\Mst87fb.
 DR INTERPRO: IPR001450; -;
 DR PROSITE: PS00198; 4FEAS_FERRDOXIN; UNKNOWN_1.
 SO SEQUENCE 49 AA; 4550 MW; 24758FEC51369F01 CRC64;

Query Match 100.0%; Score 52; DB 5; Length 49;
 Best Local Similarity 20.0%; Pred. No. 81;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXCXXXXXXXXXXC 20
 Db 23 CCGPCVSCGPGVSCCGGCC 42

RESULT 8
 ID Q9Y110 PRELIMINARY; PRT; 54 AA.

AC Q9Y110;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, last annotation update)
 DE ALPHA-BUNGAROTOXIN ISOFORM K7 (FRAGMENT).
 OS Bungarus multicinctus (Many-banded krait).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Elapidae; Bungarinae; Bungarus.
 OX NCBI_TaxID=8616;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=VENOM GLAND;
 RX MEDLINE=99058072; PubMed=9837992;
 RA Liu L.F., Chang C.C., Liu M.Y., Kuo K.W.;
 RT "Genetic characterization of the mRNAs encoding alpha-bungarotoxin:
 isoforms and RNA editing in Bungarus multicinctus gland cells.";
 RL Nucleic Acids Res. 26:5624-5629(1998).
 DR EMBL: AF056407; AAC83988.1; -;

